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SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

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<151> 2003-06-11

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 <213> Adenovirus serotype 2 fiber

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<400> 33
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1      5      10      15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
      20      25      30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
      35      40      45
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
      50      55      60
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
65      70      75      80
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
      85      90      95
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
      100      105      110
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
      115      120      125
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
      130      135      140
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145      150      155      160
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
      165      170      175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
      180      185      190
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser

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Gly	Pro	Leu	Gln	Val	Ala	Gln	Asn	Ser	Asp	Thr	Leu	205	Thr	Val	Val	Thr
Gly	210					215					220					
225	Pro	Gly	Val	Thr	Val	Glu	Gln	Asn	Ser	Leu	Arg	Thr	Lys	Val	Ala	
Gly	Ala	Ile	Gly	Tyr	Asp	Ser	Ser	Asn	Asn	Met	Glu	Ile	Lys	Thr	240	
				245					250						255	Gly
Gly	Gly	Met	Arg	Ile	Asn	Asn	Asn	Leu	Leu	Ile	Leu	Asp	Val	Asp	Tyr	
			260					265								
Pro	Phe	Asp	Ala	Gln	Thr	Lys	Leu	Arg	Leu	Lys	Leu	Gly	Gln	Gly	Pro	
		275					280									
Leu	Tyr	Ile	Asn	Ala	Ser	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	Arg	Gly	
						295					300					
Leu	Tyr	Leu	Phe	Asn	Ala	Ser	Asn	Asn	Thr	Lys	Lys	Leu	Glu	Val	Ser	
305					310										320	
Ile	Lys	Lys	Ser	Ser	Gly	Leu	Asn	Phe	Asp	Asn	Thr	Ala	Ile	Ala	Ile	
				325					330					335		
Asn	Ala	Gly	Lys	Gly	Leu	Glu	Phe	Asp	Thr	Asn	Thr	Ser	Glu	Ser	Pro	
			340					345						350		
Asp	Ile	Asn	Pro	Ile	Lys	Thr	Lys	Ile	Gly	Ser	Gly	Ile	Asp	Tyr	Asn	
		355					360					365				
Glu	Asn	Gly	Ala	Met	Ile	Thr	Lys	Leu	Gly	Ala	Gly	Leu	Ser	Phe	Asp	
						375					380					
Asn	Ser	Gly	Ala	Ile	Thr	Ile	Gly	Asn	Lys	Asn	Asp	Asp	Lys	Leu	Thr	
385					390					395					400	
Leu	Trp	Thr	Thr	Pro	Asp	Pro	Ser	Pro	Asn	Cys	Arg	Ile	His	Ser	Asp	
				405					410					415		
Asn	Asp	Cys	Lys	Phe	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Val	
			420					425						430		
Leu	Ala	Thr	Val	Ala	Ala	Leu	Ala	Val	Ser	Gly	Asp	Leu	Ser	Ser	Met	
		435					440					445				
Thr	Gly	Thr	Val	Ala	Ser	Val	Ser	Ile	Phe	Leu	Arg	Phe	Asp	Gln	Asn	
						455				460						
Gly	Val	Leu	Met	Glu	Asn	Ser	Ser	Leu	Lys	Lys	His	Tyr	Trp	Asn	Phe	
465					470					475					480	
Arg	Asn	Gly	Asn	Ser	Thr	Asn	Ala	Asn	Pro	Tyr	Thr	Asn	Ala	Val	Gly	
				485					490					495		
Phe	Met	Pro	Asn	Leu	Leu	Ala	Tyr	Pro	Lys	Thr	Gln	Ser	Gln	Thr	Ala	
			500					505					510			
Lys	Asn	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	His	Gly	Asp	Lys	Thr	Lys	
		515						520				525				
Pro	Met	Ile	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Ser	Glu	Ser	Thr	Glu	
						535					540					
Thr	Ser	Glu	Val	Ser	Thr	Tyr	Ser	Met								

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<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber
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<220>
<221> CDS
<222> (1) ... (1746)
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<400> 34

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atg Met 1	aag Lys	cgc Arg	gca Ala	aga Arg 5	ccg Pro	tct Ser	gaa Glu	gat Asp	acc Thr 10	ttc Phe	aac Asn	ccc Pro	gtg Val	tat Tyr 15	cca Pro	48
tat Tyr	gac Asp	acg Thr	gaa Glu 20	acc Thr	ggg Gly	cct Pro	cca Pro	act Thr 25	gtg Val	cct Pro	ttt Phe	ctt Leu	act Thr 30	cct Pro	ccc Pro	96
ttt Phe	gta Val	tcc Ser 35	ccc Pro	aat Asn	ggg Gly	ttt Phe	caa Gln 40	gag Glu	agt Ser	ccc Pro	cct Pro	ggg Gly 45	gta Val	ctc Leu	tct Ser	144
ttg Leu	cgc Arg 50	cta Leu	tcc Ser	gaa Glu	cct Pro	cta Leu 55	gtt Val	acc Thr	tcc Ser	aat Asn	ggc Gly 60	atg Met	ctt Leu	gcg Ala	ctc Leu	192
aaa Lys 65	atg Met	ggc Gly	aac Asn	ggc Gly	ctc Leu 70	tct Ser	ctg Leu	gac Asp	gag Glu	gcc Ala 75	ggc Gly	aac Asn	ctt Leu	acc Thr	tcc Ser 80	240
caa Gln	aat Asn	gta Val	acc Thr	act Thr 85	gtg Val	agc Ser	cca Pro	cct Pro	ctc Leu 90	aaa Lys	aaa Lys	acc Thr	aag Lys	tca Ser 95	aac Asn	288
ata Ile	aac Asn	ctg Leu	gaa Glu 100	ata Ile	tct Ser	gca Ala	ccc Pro	ctc Leu 105	aca Thr	gtt Val	acc Thr	tca Ser	gaa Glu 110	gcc Ala	cta Leu	336
act Thr	gtg Val	gct Ala 115	gcc Ala	gcc Ala	gca Ala	cct Pro	cta Leu 120	atg Met	gtc Val	gcg Ala	ggc Gly	aac Asn 125	aca Thr	ctc Leu	acc Thr	384
atg Met 130	caa Gln	tca Ser	cag Gln	gcc Ala	ccg Pro	cta Leu 135	acc Thr	gtg Val	cac His	gac Asp	tcc Ser 140	aaa Lys	ctt Leu	agc Ser	att Ile	432
gcc Ala 145	acc Thr	caa Gln	gga Gly	ccc Pro	ctc Leu 150	aca Thr	gtg Val	tca Ser	gaa Glu	gga Gly 155	aag Lys	cta Leu	gcc Ala	ctg Leu	caa Gln 160	480
aca Thr	tca Ser	ggc Gly	ccc Pro	ctc Leu 165	acc Thr	acc Thr	gat Asp	agc Ser 170	agt Ser	acc Thr	ctt Leu	act Thr	atc Ile 175	act Thr		528
gcc Ala	tca Ser	ccc Pro	cct Pro 180	cta Leu	act Thr	act Thr	gcc Ala	act Thr 185	ggg Gly	agc Ser	ttg Leu	ggc Gly	att Ile 190	gac Asp	ttg Leu	576
aaa Lys	gag Glu	ccc Pro 195	att Ile	tat Tyr	aca Thr	caa Gln	aat Asn 200	gga Gly	aaa Lys	cta Leu	gga Gly	cta Leu 205	aag Lys	tac Tyr	ggg Gly	624
gct Ala 210	cct Pro	ttg Leu	cat His	gta Val	aca Thr	gac Asp 215	gac Asp	cta Leu	aac Asn	act Thr 220	ttg Leu	acc Thr	gta Val	gca Ala	act Thr	672
ggg Gly 225	cca Pro	ggg Gly	gtg Val	act Thr	att Ile 230	aat Asn	aat Asn	act Thr	tcc Ser	ttg Leu 235	caa Gln	act Thr	aaa Lys	gtt Val	act Thr 240	720
gga Gly	gcc Pro	ttg Leu	ggg Gly	ttt Leu	gat Thr	tca Thr	caa Gln	ggc Gly	aat Thr	atg Thr	caa Gln	ctt Thr	aat Thr	gta Val	gca Ala	768

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Gly	Ala	Leu	Gly	Phe 245	Asp	Ser	Gln	Gly	Asn 250	Met	Gln	Leu	Asn	Val 255	Ala		
gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	gtt	816	
Gly	Gly	Leu	Arg 260	Ile	Asp	Ser	Gln	Asn 265	Arg	Arg	Leu	Ile	Leu 270	Asp	Val		
agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	cta	gga	cag	864	
Ser	Tyr		Phe 275	Asp	Ala	Gln	Asn 280	Gln	Leu	Asn	Leu	Arg 285	Leu	Gly	Gln		
ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	aac	tac	aac	912	
Gly	Pro 290	Leu	Phe	Ile	Asn	Ser 295	Ala	His	Asn	Leu	Asp 300	Ile	Asn	Tyr	Asn		
aaa	ggc	ctt	tac	ttg	ttt	aca	gct	tca	aac	aat	tcc	aaa	aag	ctt	gag	960	
Lys 305	Gly	Leu	Tyr	Leu	Phe 310	Thr	Ala	Ser	Asn 315	Asn	Ser	Lys	Lys	Leu	Glu 320		
gtt	aac	cta	agc	act	gcc	aag	ggg	ttg	atg	ttt	gac	gct	aca	gcc	ata	1008	
Val	Asn	Leu	Ser	Thr 325	Ala	Lys	Gly	Leu	Met 330	Phe	Asp	Ala	Thr	Ala 335	Ile		
gcc	att	aat	gca	gga	gat	ggg	ctt	gaa	ttt	ggt	tca	cct	aat	gca	cca	1056	
Ala	Ile	Asn	Ala 340	Gly	Asp	Gly	Leu	Glu 345	Phe	Gly	Ser	Pro	Asn 350	Ala	Pro		
aac	aca	aat	ccc	ctc	aaa	aca	aaa	att	ggc	cat	ggc	cta	gaa	ttt	gat	1104	
Asn	Thr	Asn 355	Pro	Leu	Lys	Thr	Lys 360	Ile	Gly	His	Gly	Leu 365	Glu	Phe	Asp		
tca	aac	aag	gct	atg	gtt	cct	aaa	cta	gga	act	ggc	ctt	agt	ttt	gac	1152	
Ser	Asn 370	Lys	Ala	Met	Val	Pro 375	Lys	Leu	Gly	Thr	Gly 380	Leu	Ser	Phe	Asp		
agc	aca	ggt	gcc	att	aca	gta	gga	aac	aaa	aat	aat	gat	aag	cta	act	1200	
Ser 385	Thr	Gly	Ala	Ile	Thr 390	Val	Gly	Asn	Lys	Asn 395	Asn	Asp	Lys	Leu	Thr 400		
ttg	tgg	acc	aca	cca	gct	cca	tct	cct	aac	tgt	aga	cta	aat	gca	gag	1248	
Leu	Trp	Thr	Thr	Pro 405	Ala	Pro	Ser	Pro	Asn 410	Cys	Arg	Leu	Asn	Ala 415	Glu		
aaa	gat	gct	aaa	ctc	act	ttg	gtc	tta	aca	aaa	tgt	ggc	agt	caa	ata	1296	
Lys	Asp	Ala 420	Lys	Leu	Thr	Leu	Val 425	Leu	Thr	Lys	Cys	Gly 430	Ser	Gln	Ile		
ctt	gct	aca	gtt	tca	gtt	ttg	gct	gtt	aaa	ggc	agt	ttg	gct	cca	ata	1344	
Leu	Ala 435	Thr	Val	Ser	Val	Leu	Ala 440	Val	Lys	Gly	Ser	Leu 445	Ala	Pro	Ile		
tct	gga	aca	gtt	caa	agt	gct	cat	ctt	att	ata	aga	ttt	gac	gaa	aat	1392	
Ser	Gly 450	Thr	Val	Gln	Ser	Ala 455	His	Leu	Ile	Ile	Arg 460	Phe	Asp	Glu	Asn		
gga	gtg	cta	cta	aac	aat	tcc	ttc	ctg	gac	cca	gaa	tat	tgg	aac	ttt	1440	
Gly 465	Val	Leu	Leu	Asn 470	Asn	Ser	Phe	Leu	Asp	Pro 475	Glu	Tyr	Trp	Asn 480	Phe		
aga	aat	gga	gat	ctt	act	gaa	ggc	aca	gcc	tat	aca	aac	gct	gtt	gga	1488	
Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly		

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485										490					495					
ttt	atg	cct	aac	cta	tca	gct	tat	cca	aaa	tct	cac	ggt	aaa	act	gcc	1536				
Phe	Met	Pro	Asn	Leu	Ser	Ala	Tyr	Pro	Lys	Ser	His	Gly	Lys	Thr	Ala					
			500					505					510							
aaa	agt	aac	att	gtc	agt	caa	gtt	tac	tta	aac	gga	gac	aaa	act	aaa	1584				
Lys	Ser	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	Asn	Gly	Asp	Lys	Thr	Lys					
		515					520					525								
cct	gta	aca	cta	acc	att	aca	cta	aac	ggt	aca	cag	gaa	aca	gga	gac	1632				
Pro	Val	Thr	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Gln	Glu	Thr	Gly	Asp					
	530					535					540									
aca	act	cca	agt	gca	tac	tct	atg	tca	ttt	tca	tgg	gac	tgg	tct	ggc	1680				
Thr	Thr	Pro	Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly					
545					550				555						560					
cac	aac	tac	att	aat	gaa	ata	ttt	gcc	aca	tcc	tct	tac	act	ttt	tca	1728				
His	Asn	Tyr	Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser					
				565				570						575						
tac	att	gcc	caa	gaa	taa											1746				
Tyr	Ile	Ala	Gln	Glu	*															
			580																	

<210> 35
 <211> 581
 <212> PRT
 <213> Adenovirus serotype 5 fiber

<400> 35

Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro
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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro
			20					25					30		
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser
	35						40					45			
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu
	50					55					60				
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser
65					70					75				80	
Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn
			85					90						95	
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu
			100					105					110		
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr
		115					120					125			
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile
	130					135					140				
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln
145					150					155				160	
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr
				165				170						175	
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu
		180						185					190		
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly
	195						200					205			
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr
	210					215					220				

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Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
 450 455 460
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
 485 490 495
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
 530 535 540
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 565 570 575
 Tyr Ile Ala Gln Glu
 580

<210> 36
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 37 fiber

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 36
 atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc 48
 Met Ser Lys Arg Leu Arg Val Glu Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15

-23-

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt	96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe	
20 25 30	
gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc	144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
35 40 45	
aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag	192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
50 55 60	
gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct	240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
65 70 75 80	
aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat	288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
85 90 95	
gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga	336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
100 105 110	
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat	384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
115 120 125	
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa	432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
130 135 140	
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta	480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
145 150 155 160	
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca	528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
165 170 175	
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca	576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
180 185 190	
tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg	624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
195 200 205	
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att	672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile	
210 215 220	
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa	720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys	
225 230 235 240	
ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt	768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu	
245 250 255	

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tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga 816
 Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
 260 265 270
 aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct 864
 Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
 275 280 285
 aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga 912
 Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
 290 295 300
 gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca 960
 Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
 305 310 315 320
 gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct 1008
 Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
 325 330 335
 atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt 1056
 Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
 340 345 350
 gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga 1098
 Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
 355 360 365

<210> 37

<211> 365

<212> PRT

<213> Adenovirus serotype 37 fiber

<400> 37

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160
 Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
 165 170 175
 Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
 180 185 190
 Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu

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      195      200      205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
  210      215      220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
  225      230      235
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
      245      250      255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
      260      265      270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
      275      280      285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
      290      295      300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
  305      310      315
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
      325      330      335
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
      340      345      350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
      355      360      365

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<210> 38
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 19p fiber

<220>
 <221> CDS
 <222> (1)...(1098)

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<400> 38
atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc   48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
  1      5      10      15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt   96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
      20      25      30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc   144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
      35      40      45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag   192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
      50      55      60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct   240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
      65      70      75      80

aag gct cca ctg caa gtt act act gat aaa ctt gag ctt gca tat   288
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Leu Glu Leu Ala Tyr
      85      90      95

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga   336
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
      100      105      110

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cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp 115 120 125	384
tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu 130 135 140	432
aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val 145 150 155 160	480
aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala 165 170 175	528
tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr 180 185 190	576
tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu 195 200 205	624
gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile 210 215 220	672
gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu 225 230 235 240	720
ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu 245 250 255	768
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly 260 265 270	816
aat tcc aat gtt tgc aca gct tat gaa aaa gca att ggt ttt atg cct Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro 275 280 285	864
aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg 290 295 300	912
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro 305 310 315 320	960
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser 325 330 335	1008
atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe 340 345 350	1056
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098

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Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
 355 360 365

<210> 39
 <211> 365
 <212> PRT
 <213> Adenovirus serotype 19p fiber

<400> 39
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160
 Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
 165 170 175
 Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
 180 185 190
 Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
 195 200 205
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
 210 215 220
 Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
 225 230 235 240
 Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
 245 250 255
 Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
 260 265 270
 Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
 275 280 285
 Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
 290 295 300
 Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
 305 310 315 320
 Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
 325 330 335
 Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
 340 345 350
 Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
 355 360 365

<210> 40
 <211> 1228

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<212> DNA

<213> Adenovirus serotype 9 fiber

<220>

<221> CDS

<222> (50) ... (1138)

<400> 40

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aagggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58
                                     Met Ser Lys
                                     1
agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac 106
Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
      5                                10
gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc 154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
      20                                25                                30
gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct 202
Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
                                     40                                45                                50
gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg 250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
                                     55                                60                                65
ggg ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat 298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
      70                                75                                80
cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct 346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
      85                                90                                95
cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc 394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
      100                                105                                110                                115
ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat 442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
      120                                125                                130
act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat 490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
      135                                140                                145
aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca 538
Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
      150                                155                                160
ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag 586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
      165                                170                                175
cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat 634
Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
      180                                185                                190                                195
cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt 682

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Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
 200 205 210
 caa ata ttg gct aat gtg tca tta att gtc gta gat ggt aag tac aaa 730
 Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly Lys Tyr Lys
 215 220
 att atc aat aac aat act caa cca gct ctc aaa gga ttt acc att aaa 778
 Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr Ile Lys
 230 235 240
 tta ttg ttt gat gaa aat gga gta ctt atg gaa tct tca aat ctt ggt 826
 Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn Leu Gly
 245 250 255
 aaa tca tat tgg aac ttt aga aat gaa aat tca att atg tca aca gct 874
 Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser Thr Ala
 260 265 270 275
 tat gaa aaa gct att gga ttc atg cct aat ttg gta gcc tat cca aaa 922
 Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys
 280 285 290
 cct acc gct ggc tct aaa aaa tat gca aga gat ata gtt tat gga aac 970
 Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Asn
 295 300 305
 atc tac ctt ggt gga aag cca gat caa cca gta acc att aaa act acc 1018
 Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys Thr Thr
 310 315 320
 ttt aat cag gaa act gga tgt gaa tat tct atc aca ttt gat ttt agt 1066
 Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp Phe Ser
 325 330 335
 tgg gcc aag act tat gta aat gtt gaa ttt gaa aca acc tct ttt acc 1114
 Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
 340 345 350 355
 ttt tcc tat atc gcc caa gaa tga aagaccaata aacgtgtttt tcattttcaaa 1168
 Phe Ser Tyr Ile Ala Gln Glu *
 360
 attttcatgt atctttattg atttttacac cagcacgggt agtcagtctc ccaccaccag 1228

<210> 41

<211> 362

<212> PRT

<213> Adenovirus serotype 9 fiber

<400> 41

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val

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65	Asn	Ala	Asp	Pro	Pro	Leu	Gln	Leu	Thr	Asn	Asn	Lys	Leu	Gly	Ile	Ala	80
	Leu	Asp	Ala	Pro	85	Phe	Asp	Val	Ile	Asp	90	Asn	Lys	Leu	Thr	Leu	Ala
	Gly	His	Gly	Leu	100	Ser	Ile	Ile	Thr	105	Lys	Glu	Thr	Ser	Thr	Leu	Ala
	Leu	Arg	Asn	Thr	115	Leu	Val	Val	Leu	120	Thr	Gly	Lys	Gly	Ile	Gly	Thr
	Ser	Thr	Asp	Asn	130	Gly	Gly	Thr	Val	135	Cys	Val	Arg	Val	Gly	Glu	Gly
	Gly	Leu	Ser	Phe	145	Asn	Asp	Gly	Asp	150	Leu	Val	Ala	Phe	Asn	Lys	Lys
	Glu	Asp	Lys	Arg	165	Thr	Leu	Trp	Thr	170	Pro	Asp	Thr	Ser	Pro	Asn	Cys
	Lys	Ile	Asp	Gln	180	Asp	Lys	Asp	Ser	185	Lys	Leu	Thr	Leu	Val	Leu	Thr
	Cys	Gly	Ser	Gln	195	Ile	Leu	Ala	Asn	200	Val	Ser	Leu	Ile	Val	Val	Asp
	Lys	Tyr	Lys	Ile	210	Ile	Asn	Asn	Asn	215	Thr	Gln	Pro	Ala	Leu	Lys	Gly
	Thr	Ile	Lys	Leu	225	Phe	Asp	Glu	Asn	230	Gly	Val	Leu	Met	Glu	Ser	Ser
	Asn	Leu	Gly	Lys	245	Ser	Tyr	Trp	Asn	250	Phe	Arg	Asn	Glu	Asn	Ser	Ile
	Ser	Thr	Ala	Tyr	260	Glu	Lys	Ala	Ile	265	Gly	Phe	Met	Pro	Asn	Leu	Val
	Tyr	Pro	Lys	Pro	275	Thr	Ala	Gly	Ser	280	Lys	Lys	Tyr	Ala	Arg	Asp	Ile
	Tyr	Gly	Asn	Ile	290	Tyr	Leu	Gly	Gly	295	Lys	Pro	Asp	Gln	Pro	Val	Thr
	Lys	Thr	Thr	Phe	305	Asn	Gln	Glu	Thr	310	Gly	Cys	Glu	Tyr	Ser	Ile	Thr
	Asp	Phe	Ser	Trp	325	Ala	Lys	Thr	Tyr	330	Val	Asn	Val	Glu	Phe	Glu	Thr
	Ser	Phe	Thr	Phe	340	Ser	Tyr	Ile	Ala	345	Gln	Glu					
					355					360							

<210> 42
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad2 third repeat

<400> 42
 Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
 1 5 10 15
 Lys Thr Lys Ser
 20

<210> 43
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5 third repeat

-31-

<400> 43

Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
 1 5 10 15
 Lys Thr Lys Ser 20

<210> 44

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Repeat motif

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ser

<400> 44

Thr Thr Val Xaa
 1

<210> 45

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Repeat Consensus Sequence

<221> VARIANT

<222> 3,5,7,13

<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT

<222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 10

<223> Xaa = Pro or Gly

<400> 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

<210> 46

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad2 21st repeat

<400> 46

Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
 1 5 10 15

-32-

<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1 5

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5Ds fiber

<221> CDS
<222> (13)...(1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G

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<400> 50

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atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
      Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
        1             5             10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
      15             20             25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
      30             35             40             45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
      50             55             60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
      65             70             75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
      80             85             90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
      95             100             105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
      110             115             120             125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
      130             135             140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
      145             150             155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat 531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
      160             165             170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt 579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
      175             180             185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa 627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Thr Val Leu Thr Lys
      190             195             200             205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc 675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
      210             215             220

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata 723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
      225             230             235

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aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca 771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro
240 245 250

gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat 819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr
255 260 265

aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct 867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser
270 275 280 285

cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac 915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn
290 295 300

gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca 963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr
305 310 315

cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca 1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser
320 325 330

tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc 1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser
335 340 345

tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa 1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *
350 355

gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca 1164

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<210> 51

<211> 359

<212> PRT

<213> Artificial Sequence

<220>

<223> Ad5deltas

<400> 51

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys
85 90 95
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr
100 105 110
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn
115 120 125
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu
130 135 140

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Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
 145 150 155 160
 Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
 165 170 175
 Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
 180 185 190
 Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
 195 200 205
 Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
 210 215 220
 Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
 225 230 235 240
 Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
 245 250 255
 Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
 260 265 270
 Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
 275 280 285
 Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Thr Gln Glu Thr
 290 295 300
 Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
 305 310 315 320
 Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
 325 330 335
 Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
 340 345 350
 Phe Ser Tyr Ile Ala Gln Glu
 355

<210> 52
 <211> 1920
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37k fiber

<221> CDS
 <222> (13)...(1755)

<221> misc_feature
 <222> 1867, 1875
 <223> n = A,T,C or G

<400> 52
 gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10
 gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25
 act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45
 gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

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ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn 65 70 75	243
ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr 80 85 90	291
aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser 95 100 105	339
gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac Glu Ala Leu Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn 110 115 120 125	387
aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys 130 135 140	435
ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu 145 150 155	483
gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu 160 165 170	531
act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly 175 180 185	579
att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu 190 195 200 205	627
aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr 210 215 220	675
gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr 225 230 235	723
aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu 240 245 250	771
aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile 255 260 265	819
ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg 270 275 280 285	867
cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile 290 295 300	915

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aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys 305 310 315	963
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala 320 325 330	1011
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro 335 340 345	1059
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu 350 355 360 365	1107
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu 370 375 380	1155
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp 385 390 395	1203
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile 400 405 410	1251
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly 415 420 425	1299
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr 430 435 440 445	1347
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile 450 455 460	1395
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu 465 470 475	1443
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr 480 485 490	1491
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro 495 500 505	1539
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr 510 515 520 525	1587
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr 530 535 540	1635
ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683

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Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
 545 550 555
 tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc 1731
 Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
 560 565 570
 ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg 1785
 Phe Ser Tyr Ile Ala Gln Glu *
 575 580
 tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttggtttgcc 1845
 cctcccccggt gccttccttg ancctggaan gtgccactcc cactgtcctt tcctaataaa 1905
 atgaggaaat gcatc 1920

<210> 53
 <211> 580
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37k

<400> 53
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 1 5 10 15
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

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290
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 310
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 325
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 340
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 355
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 370
 385
 Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp
 390
 Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 405
 Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile
 420
 Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu
 435
 Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala
 450
 465
 Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu
 485
 Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser
 500
 Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu
 515
 Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln
 530
 Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys
 545
 Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr
 565
 Ile Ala Gln Glu
 580

<210> 54
 <211> 1767
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s fiber

<221> CDS
 <222> (13)...(1749)

<400> 54
 atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10
 gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25
 act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly

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30	35	40	45	
gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met 50 55 60				195
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser 65 70 75				243
cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn 80 85 90				291
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 95 100 105				339
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 110 115 120 125				387
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130 135 140				435
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145 150 155				483
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 160 165 170				531
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 175 180 185				579
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 190 195 200 205				627
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210 215 220				675
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225 230 235				723
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 240 245 250				771
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 255 260 265				819
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 270 275 280 285				867

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ggc cct ctt ttt Gly Pro Leu Phe	ata aac tca gcc cac Ile Asn Ser Ala His	aac ttg gat att Asn Leu Asp Ile	aac tac aac Asn Tyr Asn	915
aaa ggc ctt tac Lys Gly Leu Tyr	ttg ttt aca gct tca Leu Phe Thr Ala Ser	aac aat tcc aaa Asn Asn Ser Lys	aag ctt gag Lys Leu Glu	963
gtt aac cta agc act Val Asn Leu Ser	gcc aag ggg ttg atg Ala Lys Gly Leu	ttt gac gct aca Phe Asp Ala Thr	gcc ata Ala Ile	1011
gcc att aat gca gga Ala Ile Asn Ala	gat ggg ctt gaa ttt Asp Gly Leu Glu	ggg tca cct aat Gly Ser Pro Asn	gca cca Ala Pro	1059
aac aca aat ccc ctc Asn Thr Asn Pro	aaa aca aaa att Lys Thr Lys Ile	ggc cat ggc cta Gly His Gly Leu	gaa ttt gat Glu Phe Asp	1107
tca aac att ggt ata Ser Asn Ile Gly	aat gta aga gca Asn Val Arg Ala	aga gaa ggg ttg Arg Glu Gly Leu	aca ttt gac Thr Phe Asp	1155
aat gat ggt gcc att Asn Asp Gly Ala	aca gta gga aac Ile Thr Val Gly	aaa aat aat gat Lys Asn Asn Asp	aag cta act Lys Leu Thr	1203
ttg tgg acc aca cca Leu Trp Thr Pro	gct cca tct cct Ala Pro Ser Pro	aac tgt aga cta Asn Cys Arg Leu	aat gca gag Asn Ala Glu	1251
aaa gat gct aaa ctc Lys Asp Ala Lys	act ttg gtc tta Thr Leu Val Leu	aca aaa tgt ggc Thr Lys Cys Gly	agt caa ata Ser Gln Ile	1299
ctt gct aca gtt tca Leu Ala Thr Val	ggt ttg gct gtt Val Leu Ala Val	aaa ggc agt ttg Lys Gly Ser Leu	gct cca ata Ala Pro Ile	1347
tct gga aca gtt caa Ser Gly Thr Val	agt gct cat ctt Ser Ala His Leu	att ata aga ttt Ile Ile Arg Phe	gac gaa aat Asp Glu Asn	1395
gga gtg cta cta aac Gly Val Leu Leu	aat tcc ttc ctg Asn Asn Ser Phe	gac cca gaa tat Asp Pro Glu Tyr	tgg aac ttt Trp Asn Phe	1443
aga aat gga gat ctt Arg Asn Gly Asp	act gaa ggc aca Thr Glu Gly Thr	gcc tat aca aac Ala Tyr Thr Asn	gct gtt gga Ala Val Gly	1491
ttt atg cct aac cta Phe Met Pro Asn	tca gct tat cca Leu Ser Ala Pro	aaa tct cac ggt Lys Ser His Gly	aaa act gcc Lys Thr Ala	1539
aaa agt aac att gtc Lys Ser Asn Ile	agc agt caa gtt Val Ser Gln Val	tac tta aac gga Tyr Leu Asn Gly	gac aaa act Asp Lys Thr	1587

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cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
      530      535      540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
      545      550      555

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
      560      565      570

tac att gcc caa gaa taa agaagcggcc gcgttatg 1767
Tyr Ile Ala Gln Glu *
      575

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<210> 55
 <211> 578
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s

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<400> 55
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1      5      10      15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
      20      25      30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
      35      40      45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
      50      55      60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val
      65      70      75      80
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu
      85      90      95
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala
      100      105      110
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser
      115      120      125
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln
      130      135      140
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly
      145      150      155      160
Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro
      165      170      175
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro
      180      185      190
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu
      195      200      205
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly
      210      215      220
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu
      225      230      235      240
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu
      245      250      255
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro
      260      265      270
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu

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275
 Phe Ile Asn Ser Ala His Asn 280
 290 295
 Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys 285
 305 310 315
 Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile Ala Ile Asn
 325 330 335
 Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Asn Thr Asn
 340 345 350
 Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp Ser Asn Ile
 355 360 365
 Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
 370 375 380
 Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr Leu Trp Thr
 385 390 395
 Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
 405 410 415
 Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
 420 425 430
 Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
 435 440 445
 Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
 450 455 460
 Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
 465 470 475
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
 485 490 495
 Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
 500 505 510
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
 515 520 525
 Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
 530 535 540
 Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
 545 550 555
 Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
 565 570 575
 Gln Glu

<210> 56
 <211> 1132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k fiber

<221> CDS
 <222> (16) ... (1116)

<221> misc_feature
 <222> 1125
 <223> n = A,T,C or G

<400> 56
 gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
 1 5 10

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ccc gtc tac ccc tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu 15 20 25	99
act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly 30 35 40	147
gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp 45 50 55 60	195
gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu 65 70 75	243
act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu 80 85 90	291
gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser 95 100 105	339
tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala 110 115 120	387
ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly 125 130 135 140	435
ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile 145 150 155	483
ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly 160 165 170	531
tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr 175 180 185	579
aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala 190 195 200	627
aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr 205 210 215 220	675
gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr 225 230 235	723
gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu 240 245 250	771
cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga	819

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Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
 255 260 265
 gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct 867
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
 270 275 280
 aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac 915
 Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
 285 290 295 300
 att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca 963
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
 305 310 315
 cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca 1011
 Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
 320 325 330
 agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac 1059
 Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
 335 340 345
 att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc 1107
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 Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
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 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
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<400> 60

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<223> Penton region

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